

SEQUENCE LISTING

<110> Medlock, Eugene
Yeh, Richard
Silbiger, Scott M.
Elliot, Gary S.
Nguyen, Hung Q.
Jing, Shuqian

<120> IL-17 Like Molecules and Uses Thereof

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<151> 2001-06-21

<150> 09/810,384

<151> 2001-03-16

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<151> 2001-02-02

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Pub. No. 6,440,000

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Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe Ala Glu
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Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu Thr Ala
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Exon 1

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accctggaag ccatactcct ggctccttcc cctgaatcc cccaactcct ggcacaggca 1317

ctttctccac ctctccccct ttgccttttg ttgtgtttgt ttgtgcatgc caactctgcg 1377

tgcagccagg tgtaattgcc ttgaaggatg gttctgaggt gaaagctggt atcgaaagtg 1437

aagagattta tccaaataaa catctgtggt taaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1496

<210> 10
<211> 159
<212> PRT
<213> Mus musculus

<400> 10
Met Ile Val Gly Thr His Thr Val Ser Leu Arg Ile Gln Glu Gly Cys
1 5 10 15

Ser His Leu Pro Ser Cys Cys Pro Ser Lys Glu Gln Glu Pro Pro Glu
20 25 30

Glu Trp Leu Lys Trp Ser Ser Ala Ser Val Ser Pro Pro Glu Pro Leu
35 40 45

Ser His Thr His His Ala Glu Ser Cys Arg Ala Ser Lys Asp Gly Pro
50 55 60

Leu Asn Ser Arg Ala Ile Ser Pro Trp Ser Tyr Glu Leu Asp Arg Asp
65 70 75 80

Leu Asn Arg Val Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro
85 90 95

Sub-A1

His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Leu Gly Asn
100 105 110

Ser Val Pro Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys
115 120 125

His Gly Glu Glu Gly Thr His Arg Arg Tyr Cys Leu Glu Arg Arg Leu
130 135 140

Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met
145 150 155

<210> 11

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Epogen signal peptide

<400> 11

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly
20 25

<210> 12

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide of Fc fragment

<400> 12

Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Ref. A1

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 13
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide of HIV
TAT protein

<400> 13
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 14
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide of HIV
TAT protein

<400> 14
Phe Ile Thr Cys Gly Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln
1 5 10 15

Arg Arg Arg

<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

Sub A1

<400> 15
tagggccagt gaagatgg 18

<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 16
tacagcctgc gctccaggca gtagcc 26

<210> 17
<211> 1841
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (50)..(1555)

<400> 17
ataaaagcgc agcgtgcggg tggcctggat cccgcgcagt ggcccggcg atg tcg ctc 58
Met Ser Leu
1

gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc gta ccc cga gag 106
Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu
5 10 15

ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154
Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met
20 25 30 35

cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202
Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu
40 45 50

cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250
Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn
55 60 65

gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298
Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala
70 75 80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt 346
Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser Tyr Ser Cys
85 90 95

gtg agg tgc aat tac aca gag gcc ttc cag act cag acc aga ccc tct 394
Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr Arg Pro Ser
100 105 110 115

ggg ggt aaa tgg aca ttt tcc tac atc ggc ttc cct gta gag ctg aac 442
Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn
120 125 130

Sub-A1
1632200

aca gtc tat ttc att ggg gcc cat aat att cct aat gca aat atg aat	490
Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn	
135 140 145	
gaa gat ggc cct tcc atg tct gtg aat ttc acc tca cca ggc tgc cta	538
Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu	
150 155 160	
gac cac ata atg aaa tat aaa aaa aag tgt gtc aag gcc gga agc ctg	586
Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu	
165 170 175	
tgg gat ccg aac atc act gct tgt aag aag aat gag gag aca gta gaa	634
Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu	
180 185 190 195	
gtg aac ttc aca acc act ccc ctg gga aac aga tac atg gct ctt atc	682
Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile	
200 205 210	
caa cac agc act atc atc ggg ttt tct cag gtg ttt gag cca cac cag	730
Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln	
215 220 225	
aag aaa caa acg cga gct tca gtg gtg att cca gtg act ggg gat agt	778
Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser	
230 235 240	
gaa ggt gct acg gtg cag ctg act cca tat ttt cct act tgt ggc agc	826
Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser	
245 250 255	
gac tgc atc cga cat aaa gga aca gtt gtg ctc tgc cca caa aca ggc	874
Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly	
260 265 270 275	
gtc cct ttc cct ctg gat aac aac aaa agc aag ccg gga ggc tgg ctg	922
Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu	
280 285 290	
cct ctc ctc ctg ctg tct ctg ctg gtg gcc ada tgg gtg ctg gtg gca	970
Pro Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala	
295 300 305	
ggg atc tat cta atg tgg agg cac gaa agg atc aag aag act tcc ttt	1018
Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe	
310 315 320	
tct acc acc aca cta ctg ccc ccc att aag gtt ctt gtg gtt tac cca	1066
Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro	
325 330 335	
tct gaa ata tgt ttc cat cac aca att tgt tac ttc act gaa ttt ctt	1114
Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu	
340 345 350 355	
caa aac cat tgc aga agt gag gtc atc ctc gaa aag tgg cag aaa aag	1162
Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys	
360 365 370	

Put A/

aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc act caa aag aag 1210
Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys
375 380 385

gca gca gac aaa gtc gtc ttc ctt ctt tcc aat gac gtc aac agt gtg 1258
Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val
390 395 400

tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc agt gag aac tct 1306
Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser
405 410 415

caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc agt gat cta aga 1354
Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg
420 425 430 435

agc cag att cat ctg cac aaa tac gtg gtg gtc tac ttt aga gag att 1402
Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile
440 445 450

gat aca aaa gac gat tac aat gct ctc agt gtc tgc ccc aag tac cac 1450
Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His
455 460 465

ctc atg aag gat gcc act gct ttc tgt gca gaa ctt ctc cat gtc aag 1498
Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys
470 475 480

cag cag gtg tca gca gga aaa aga tca caa gcc tgc cac gat ggc tgc 1546
Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys
485 490 495

tgc tcc ttg tagccccccc atgagaagca agagacctta aaggcttcct 1595
Cys Ser Leu
500

atccccaccaa ttacagggaa aaaacgtgtg atgatccga agcttactat gcagcctaca 1655

aacagcctta gtaattaaaa cattttatac caataaaatt ttcaaatatt gctaactaat 1715

gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt tatacataga 1775

aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca ataaagcatc 1835

ttcagc 1841

<210> 18
<211> 502
<212> PRT
<213> Homo sapiens

<400> 18
Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
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Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

1210
1258
1306
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1402
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1715
1775
1835
1841

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
100 105 110

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
115 120 125

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
130 135 140

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
145 150 155 160

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
165 170 175

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
180 185 190

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
195 200 205

Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
210 215 220

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
225 230 235 240

Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
245 250 255

Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
260 265 270

Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
275 280 285

Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
290 295 300

Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
305 310 315 320

Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
325 330 335

Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
340 345 350

Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
355 360 365

Sub A1

Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
370 375 380

Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
385 390 395 400

Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
405 410 415

Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
420 425 430

Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
435 440 445

Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
450 455 460

Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
465 470 475 480

His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His
485 490 495

Asp Gly Cys Cys Ser Leu
500

<210> 19
<211> 2015
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (50)..(1729)

<400> 19
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Met Ser Leu
1

gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc gta ccc cga gag 106
Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu
5 10 15

ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154
Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met
20 25 30 35

cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202
Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu
40 45 50

cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250
Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn
55 60 65

gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298
Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala
70 75 80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt 346

Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser	Tyr	Ser	Cys	
	85					90					95					
gtg	agg	ctg	gag	tgc	agt	ggg	ggg	atc	atg	gct	cgc	tgc	gac	ctc	aat	394
Val	Arg	Leu	Glu	Cys	Ser	Gly	Ala	Ile	Met	Ala	Arg	Cys	Asp	Leu	Asn	
100					105					110					115	
ctt	ctg	ggc	tca	agc	gat	cgt	tct	gct	tca	gcc	tcc	cga	gcg	gct	ggg	442
Leu	Leu	Gly	Ser	Ser	Asp	Arg	Ser	Ala	Ser	Ala	Ser	Arg	Ala	Ala	Gly	
				120					125					130		
act	gca	ggc	gtg	ggc	cac	cag	acc	tgg	cta	att	ttt	gta	gtt	ttt	gta	490
Thr	Ala	Gly	Val	Gly	His	Gln	Thr	Trp	Leu	Ile	Phe	Val	Val	Phe	Val	
			135					140					145			
gag	ggg	ggg	ttc	acc	gtg	ttg	ctg	gtc	ttg	aat	tcc	agt	gct	cag	gcg	538
Glu	Gly	Gly	Phe	Thr	Val	Leu	Leu	Val	Leu	Asn	Ser	Ser	Ala	Gln	Ala	
		150					155					160				
atc	tgc	ctg	cct	cgg	ctt	ccc	aaa	gtg	ctg	gga	tta	cag	tgg	aca	ttt	586
Ile	Cys	Leu	Pro	Arg	Leu	Pro	Lys	Val	Leu	Gly	Leu	Gln	Trp	Thr	Phe	
	165					170					175					
tcc	tac	atc	ggc	ttc	cct	gta	gag	ctg	aac	aca	gtc	tat	ttc	att	ggg	634
Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn	Thr	Val	Tyr	Phe	Ile	Gly	
180					185					190					195	
gcc	cat	aat	att	cct	aat	gca	aat	atg	aat	gaa	gat	ggc	cct	tcc	atg	682
Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn	Glu	Asp	Gly	Pro	Ser	Met	
				200					205					210		
tct	gtg	aat	ttc	acc	tca	cca	ggc	tgc	cta	gac	cac	ata	atg	aaa	tat	730
Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu	Asp	His	Ile	Met	Lys	Tyr	
			215					220					225			
aaa	aaa	aag	tgt	gtc	aag	gcc	gga	agc	ctg	tgg	gat	ccg	aac	atc	act	778
Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	
		230					235					240				
gct	tgt	aag	aag	aat	gag	gag	aca	gta	gaa	gtg	aac	ttc	aca	acc	act	826
Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	Val	Asn	Phe	Thr	Thr	Thr	
	245					250					255					
ccc	ctg	gga	aac	aga	tac	atg	gct	ctt	atc	caa	cac	agc	act	atc	atc	874
Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile	Gln	His	Ser	Thr	Ile	Ile	
260					265					270					275	
ggg	ttt	tct	cag	gtg	ttt	gag	cca	cac	cag	aag	aaa	caa	acg	cga	gct	922
Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln	Lys	Lys	Gln	Thr	Arg	Ala	
				280					285					290		
tca	gtg	gtg	att	cca	gtg	act	ggg	gat	agt	gaa	ggg	gct	acg	gtg	cag	970
Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln	
			295				300						305			
ctg	act	cca	tat	ttt	cct	act	tgt	ggc	agc	gac	tgc	atc	cga	cat	aaa	1018
Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser	Asp	Cys	Ile	Arg	His	Lys	
		310					315					320				
gga	aca	gtt	gtg	ctc	tgc	cca	caa	aca	ggc	gtc	cct	ttc	cct	ctg	gat	1066
Gly	Thr	Val	Val	Leu	Cys	Pro	Gln	Thr	Gly	Val	Pro	Phe	Pro	Leu	Asp	
	325					330					335					

aac aac aaa agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct 1114
 Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Ser
 340 345 350 355
 ctg ctg gtg gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg 1162
 Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp
 360 365 370
 agg cac gaa agg atc aag aag act tcc ttt tct acc acc aca cta ctg 1210
 Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu
 375 380 385
 ccc ccc att aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat 1258
 Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His
 390 395 400
 cac aca att tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt 1306
 His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser
 405 410 415
 gag gtc atc ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt 1354
 Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly
 420 425 430 435
 cca gtg cag tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc 1402
 Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val
 440 445 450
 ttc ctt ctt tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc 1450
 Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly
 455 460 465
 aag agc gag ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt 1498
 Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu
 470 475 480
 gcc ttt aac ctt ttc tgc agt gat cta aga agc cag att cat ctg cac 1546
 Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His
 485 490 495
 aaa tac gtg gtg gtc tac ttt aga gag att gat aca aaa gac gat tac 1594
 Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr
 500 505 510 515
 aat gct ctc agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act 1642
 Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr
 520 525 530
 gct ttc tgt gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga 1690
 Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly
 535 540 545
 aaa aga tca caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccaccc 1739
 Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu
 550 555 560
 atgagaagca agagacctta aaggcttccct atcccaccaa ttacagggaa aaaacgtgtg 1799
 atgatcctga agcttactat gcagcctaca aacagcctta gtaattaaaa cattttatac 1859
 caataaaatt ttcaaatatt gctaactaat gtagcattaa ctaacgattg gaaactacat 1919

But AL
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 1799
 1859
 1919

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accattttga taatgcaaca ataaagcattc ttcagc 2015

<210> 20
<211> 560
<212> PRT
<213> Homo sapiens

<400> 20
Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15
Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30
Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45
Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60
Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80
Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95
Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys
100 105 110
Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg
115 120 125
Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val
130 135 140
Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser
145 150 155 160
Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln
165 170 175
Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr
180 185 190
Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly
195 200 205
Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile
210 215 220
Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro
225 230 235 240
Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe
245 250 255
Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser
260 265 270

2015
1979

Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln
275 280 285

Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala
290 295 300

Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile
305 310 315 320

Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe
325 330 335

Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu
340 345 350

Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr
355 360 365

Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr
370 375 380

Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile
385 390 395 400

Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His
405 410 415

Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala
420 425 430

Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp
435 440 445

Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly
450 455 460

Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu
465 470 475 480

Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile
485 490 495

His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys
500 505 510

Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys
515 520 525

Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val
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Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu
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<210> 21
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<212> PRT
<213> Homo sapiens

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Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
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Glu	Trp	Met	Leu	Gln	His	Asp	Leu	Ile	Pro	Gly	Asp	Leu	Arg	Asp	Leu
		35					40					45			
Arg	Val	Glu	Pro	Val	Thr	Thr	Ser	Val	Ala	Thr	Gly	Asp	Tyr	Ser	Ile
		50				55					60				
Leu	Met	Asn	Val	Ser	Trp	Val	Leu	Arg	Ala	Asp	Ala	Ser	Ile	Arg	Leu
	65				70					75					80
Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser
				85					90					95	
Tyr	Ser	Cys	Val	Arg	Cys	Asn	Tyr	Thr	Glu	Ala	Phe	Gln	Thr	Gln	Ser
			100					105					110		
Gly	Gly	Lys	Trp	Thr	Phe	Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn
		115					120					125			
Thr	Val	Tyr	Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn
	130					135					140				
Glu	Asp	Gly	Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu
	145				150					155					160
Asp	His	Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu
				165					170					175	
Trp	Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu
			180					185					190		
Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile
		195					200					205			
Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln
	210					215					220				
Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser
	225				230					235					240
Glu	Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser
				245					250					255	
Asp	Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	Pro	Gln	Thr	Gly
			260					265					270		
Val	Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	Gly	Trp	Leu
		275					280					285			
Pro	Ala	Ala	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro
	290					295					300				
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
	305				310					315				320	
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
				325					330					335	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
			340					345					350		

Protein Data Bank

Pub 10

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
355 360 365

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
370 375 380

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
385 390 395 400

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
405 410 415

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
420 425 430

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
435 440 445

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
450 455 460

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
465 470 475 480

Phe Phe Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
485 490 495

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
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Lys Ser Leu Ser Leu Ser Pro Gly Lys
515 520

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<213> Homo sapiens

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Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
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Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys
100 105 110

Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg
115 120 125

20-21-22-23-24-25-26-27-28-29-30-31-32-33-34-35-36-37-38-39-40-41-42-43-44-45-46-47-48-49-50-51-52-53-54-55-56-57-58-59-60-61-62-63-64-65-66-67-68-69-70-71-72-73-74-75-76-77-78-79-80-81-82-83-84-85-86-87-88-89-90-91-92-93-94-95-96-97-98-99-100-101-102-103-104-105-106-107-108-109-110-111-112-113-114-115-116-117-118-119-120-121-122-123-124-125-126-127-128-129-130-131-132-133-134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000

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Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser
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Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln
165 170 175

Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr
180 185 190

Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly
195 200 205

Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile
210 215 220

Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro
225 230 235 240

Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe
245 250 255

Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser
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Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln
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Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala
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Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile
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Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe
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Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Ala Ala
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Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
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Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
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Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
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Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
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Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
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Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
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Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
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But 100

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
465 470 475 480

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
485 490 495

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
500 505 510

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
515 520 525

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
530 535 540

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
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Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
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Lys Ser Leu Ser Leu Ser Pro Gly Lys
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23

24-21